This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:
(i) APPLICANT: ANDERTON, STEPHEN MARK
VAN DER ZEE, RUURD
VAN EDEN, WILLEM
(ii) TITLE OF INVENTION: PEPTIDE FRAGMENTS OF MICROBIAL STRESS PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES
(iii) NUMBER OF SEQUENCES: 6
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: THE WEBB LAW FIRM
(B) STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
(C) CITY: PITTSBURGH
(D) STATE: PENNSYLVANIA
(E) COUNTRY: UNITED STATES OF AMERICA
(F) ZIP: 15219-1818
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5" FLOPPY DISK
(B) COMPUTER: DIGITAL VENTURIS GL 6200
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: MICROSOFT WORD 2.0c
(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/716,169
(B) FILING DATE: 18-SEP-1996
(C) CLASSIFICATION:
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/NL95/00108
(B) FILING DATE: 21-MAR-1995
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: UNKNOWN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu
1               5                  10                  15

Glu Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu
            20                  25                  30

Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala
        35                  40                  45

Pro Thr Ile Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu
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                    50                  55                  60

L u Glu Asp Pro Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu
                    65                  70                  75

Val Ala Lys Lys Thr Asp Asp Val Ala Gly Asp Gly Thr Thr Thr
                    80                  85                  90

Ala Thr Val Leu Ala Gln Ala Leu Val Arg Glu Gly Leu Arg Asn
                    95                  100                 105

Val Ala Ala Gly Ala Asn Pro Leu Gly Val Lys Arg Gly Ile Glu
                    110                 115                 120

Lys Ala Val Glu Lys Val Thr Glu Thr Leu Leu Lys Gly Ala Lys
                    125                 130                 135

Glu Val Glu Thr Lys Glu Gln Ile Ala Ala Thr Ala Ala Ile Ser
                    140                 145                 150

Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile Ala Glu Ala Met Asp
                    155                 160                 165

Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu Glu Ser Asn Thr
                    170                 175                 180

Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg Phe Asp Lys
                    185                 190                 195

Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Pro Glu Arg Gln Glu
                    200                 205                 210

Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys Val
                    215                 220                 225

Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gly
                    230                 235                 240

Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu
                    245                 250                 255

Ala Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys
                    260                 265                 270

Ser Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala
                    275                 280                 285

Met Leu Gln Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser
                    290                 295                 300

Glu Glu Val Gly Leu Thr Leu Glu Asn Ala Asp Leu Ser Leu Leu
                    305                 310                 315
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100  Gly Lys Ala Arg Lys Val Val Val Thr Lys Asp Glu Thr Thr Ile
101                  320                 325                 330
102
103  Val Glu Gly Ala Gly Asp Thr Asp Ala Ile Ala Gly Arg Val Ala
104                  335                 340                 345
105
106  Gln Ile Arg Gln Glu Ile Glu Asn Ser Asp Ser Asp Tyr Asp Arg
107                  350                 355                 360
108
109  Glu Lys Leu Gln Glu Arg Leu Ala Lys Leu Ala Gly Gly Val Ala
110                  365                 370                 375
111
112  Val Ile Lys Ala Gly Ala Ala Thr Glu Val Glu Leu Lys Glu Arg
113                  380                 385                 390
114
115  Lys His Arg Ile Glu Asp Ala Val Arg Asn Ala Lys Ala Ala Val
116                  395                 400                 405
117
118  Glu Glu Gly Ile Val Ala Gly Gly Gly Val Thr Leu Leu Gln Ala
119                  410                 415                 420
120
121  Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp Glu Ala Thr
122                  425                 430                 435
123
124  Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu Lys Gln
125                  440                 445                 450
126
127  Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu Lys
128                  455                 460                 465
129
130  Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly
131                  470                 475                 480
132
133  Val Lys Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys
134                  485                 490                 495
135
136  Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu
137                  500                 505                 510
138
139  Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu
140                  515                 520                 525
141
142  Lys Ala Ser Val Pro Gly Gly Gly Asp Met Gly Gly Met Asp Phe
143                  530                 535                 540
144
145  (2) INFORMATION FOR SEQ ID NO: 2:
146  (i) SEQUENCE CHARACTERISTICS:
147  (A) LENGTH: 333
148  (B) TYPE: AMINO ACID
149  (C) STRANDEDNESS: SINGLE
150  (D) TOPOLOGY: UNKNOWN
151  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
152  Ala Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
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1               5                   10                  15

Val Phe Arg Ala Ala Leu Lys Asn Pro Asp Ile Glu Val Val Ala
                20                  25                  30

Val Asn Asp Leu Thr Asp Ala Asn Thr Leu Ala His Leu Leu Lys
                35                  40                  45

Tyr Asp Ser Val His Gly Arg Leu Asp Ala Glu Val Ser Val Asn
                50                  55                  60

Gly Asn Asn Leu Val Val Asn Gly Lys Glu Ile Ile Val Lys Ala
                65                  70                  75

Glu Arg Asp Pro Glu Asn Leu Ala Trp Gly Glu Ile Gly Val Asp
                80                  85                  90

Ile Val Val Glu Ser Thr Gly Arg Phe Thr Lys Arg Glu Asp Ala
                95                  100                 105

Ala Lys His Leu Glu Ala Gly Ala Lys Lys Val Ile Ile Ser Ala
                110                 115                 120

Pro Ala Lys Asn Glu Asp Ile Thr Ile Val Met Gly Val Asn Gln
                125                 130                 135

Asp Lys Tyr Asp Pro Lys Ala His His Val Ile Ser Asn Ala Ser
                140                 145                 150

Cys Thr Thr Asn Cys Leu Ala Pro Phe Ala Lys Val Leu His Glu
                155                 160                 165

Gln Phe Gly Ile Val Arg Gly Met Met Thr Thr Val His Ser Tyr
                170                 175                 180

Thr Asn Asp Gln Arg Ile Leu Asp Leu Pro His Lys Asp Leu Arg
                185                 190                 195

Arg Ala Arg Ala Ala Ala Glu Ser Ile Ile Pro Thr Thr Thr Gly
                200                 205                 210

Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys
                215                 220                 225

Leu Asn Gly Met Ala Met Arg Val Pro Thr Pro Asn Val Ser Val
                230                 235                 240

Val Asp Leu Val Ala Glu Leu Glu Lys Glu Val Thr Val Glu Glu
                245                 250                 255

Val Asn Ala Ala Leu Lys Ala Ala Ala Glu Gly Glu Leu Lys Gly
                260                 265                 270
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Ile Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Arg Asp Tyr Asn
                275                 280                 285

Gly Ser Thr Val Ser Ser Thr Ile Asp Ala Leu Ser Thr Met Val
                290                 295                 300

Ile Asp Gly Lys Met Val Lys Val Val Ser Trp Tyr Asp Asn Glu
                305                 310                 315

Thr Gly Tyr Ser His Arg Val Val Asp Leu Ala Ala Tyr Ile Ala
                320                 325                 330

Ser Lys Gly

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: UNKNOWN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val
1               5                   10                  15

Thr Arg Ala Ala Phe Ser Cys Asp Lys Val Asp Ile Val Ala Ile
                20                  25                  30

Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
                35                  40                  45

Tyr Asp Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu
                50                  55                  60

Asn Gly Lys Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln
                65                  70                  75

Glu Arg Asp Pro Val Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu
                80                  85                  90

Tyr Val Val Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala
                95                  100                 105

Gly Ala His Leu Lys Gly Gly Ala Lys Arg Val Ile Ile Ser Ala
                110                 115                 120

Pro Ser Ala Asp Ala Pro Met Phe Val Met Gly Val Asn His Glu
                125                 130                 135

Lys Tyr Asp Asn Ser Leu Lys Ile Val Ser Asn Ala Ser Cys Thr
                140                 145                 150

Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp Asn Phe
                155                 160                 165
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/716,169B*

DATE: 06/27/97
TIME: 13:50:12

INPUT SET: S18663.raw

Line	Error	Original Text